Title: "13245, A Novel Human Myotonic Dystrophy Type Protein Kinase and Uses Therefor"
Inventors: Rosana Kapeller-Libermann et al.
U.S. Patent Appl. No.: Not Yet Assigned
Express Mail # EL916936451US Attorney Docket No. 10147-57U1 Cust # 570

15 45	35 105	55 165	75 225	1/25 5 5 8 N	115 345	135 405	155 465
GGT	P CCA	CTC	N AAC	K AAG	R AGA	₽ GCC	P
A GCT	K AAA	A GCC	S AGC	A GCA	V GTA	L TTG	S AGC
D GAT (	G GGG	D GAT	V GTG	S TCG	V GTG	L TTA	T ACA
L TTG G	Q CAG	L TTA	H CAC	P CCT	Q CAG	A GCT	S AGC
P CCT T	FTTC	I ATA	K AAG	Q CAG	V GTG	K AAG	R CGA
N AAT C	F	G GGG	I ATT	L	E GAA	K AAG	S TCT
R CGG A	$_{ m CTG}$	E GAA	K AAG	E GAG	A GCT	K AAG	L TTA
A GCG C	N AAT	R CGA	MATG	Q CAG	FTTT	M ATG	I ATA
GGA G	L	S	L	L TTA	H CAC	V GTG	N AAC
Y TAT G	R AGG	L	A GCT	E GAG	GGT	K AAA	R CGG
K AAA T	S	P CCT	P CCT	A GCT	$^{ m C}_{ m TGT}$	M ATG	E GAG
F TTC A	A GCC	S TCT	Q CAG	I ATA	GGT	A GCT	E GAA
K AAG T	R CGG	M ATG	S AGT	ACC	V GTA	Y TAT	E
L . TTG A	S AGC	Q CAG	C	D GAC	L	I ATC	F
M ATG T	A GCC	Q CAG	E GAA	S TCC	S AGT	D GAC	F
	I ATT	O CAA	E GAA	Y TAT	R AGA	GGG	S TCA
3666	P CCC	TACT	FTTT	K AAG	V GTC	T ACC	V GTT
CAGT	E GAA	MATG	CIC	R	E GAA	A GCA	Q CAG
CCCC	A GCT (	F TTT 1	V GTT	V GTC (	TTC (	K AAA (	E GAG
AGAGCCGCCAGTGGGGAG	A GCT (	P CCC 7	F TTT (	F TTT (	D GAC	E GAG	Q CAG

# Fig. 1A

175 525	195 585	215 645	235 705	2/25 595 2/25 2/25	275 825	295 885	315 945
E GAA	E GAA	M ATG	I ATC	K AAA	D GAT	EGAG	I ATT
E GAG	D GAT	L	H CAC	A GCC	ტ ტტ	Y TAT	N AAC
M ATG	$_{ m TTA}$	H CAT	G GGA	N AAT	N AAC	A GCC	N AAT
L	Q CAG	V GTT	T ACA	V GTG	M ATG	I ATT	F
Y TAT	D GAC	S AGC	R CGC	M ATG	V GTG	V GTG	T ACC
LCTT	E GAG	H CAC	D GAC	K AAG	T ACT	C CC CC	R AGA
H CAC	Y TAT	V GTT	V GTT	N AAC	L	V GTG	A GCC
N AAT	R AGA	A GCT	L	S TCA	V GTG	S TCA	S
K AAA	N AAT	$^{ m L}_{ m TTG}$	I ATT	N AAT	E GAA	W TGG	TACC
D GAC	L TTG	I ATT	N AAC	M ATG	P CCT	W TGG	G GGA
Q CAG	L	L	E GAG	K AAA	A GCT	D GAC	E GAG
F	S TCA	E GAG	P CCT	A GCG	M ATG	$^{ m C}_{ m TGT}$	A GCA
A GCC	L CTG	A GCT	K AAG	A GCC	Y TAC	D GAC	F
Y TAT	L TTG	L CTA	I ATC	S TCT	D GAT	$_{ m L}$	CCC
Q CAG	D GAC	Y TAC	D GAC	G GGA	P CCA	9 99	S
L TTA	G GGG	H H H H	R CGA	F F F	T ACC	Y TAC	R AGA
Q CAA	G GGA	Q CAG	H CAT	D GAT	999	T ACC	999
P	P CCT	I ATA	V GTG	V GTG	I ATT	g ggc	Y TAT
I ATC	Q CAG	L	Y TAC	L CTG	P	K AAA	I ATT
W TGG	Y TAT	N AAC	G GGA	K AAG	CIC	G GGA	MATG

## Fig. 11

335 005	355 )65	375	395	3/25	135	155 365	175
3	3	11	11	4 12	13	4 13	14
L CTT	C	F	S TCG	P CCG	V GTG	S AGC	$_{ m L}$
F T T T T	L	PCCC	N AAT	L	V GTT	K AAA	R CGG
D GAC	G GGT	CCC	K AAG	E GAA	S TCT	I ATC	T ACC
S AGT	E GAA	P CCT	E GAG	E GAA	E GAG	L	M ATG
S AGC	F T T T	S TCT	P CCA	G GGT	S TCT	$_{ m CTT}$	E GAA
V GTG	K AAG	N AAC	E GAA	S TCG	R AGA	K AAA	Q CAG
K AAA	L CIG	R CGT	D GAT	FTC	G	K AAG	E GAG
P CCC	R AGA	I ATT	F TTT	G GGC	L	E GAA	M ATG
D GAC	E GAG	N AAC	N AAT	s TCA	I ATT	M ATG	K AAG
D GAT	K AAA	N AAC	S TCC	P	G GGG	S	H CAC
P CCA	Q CAG	W	T ACC	S AGC	L CIG	S AGC	$_{\mathtt{TGT}}^{\mathtt{C}}$
F TTT	GGC	D GAC	D GAC	L CTG	A GCA	TACT	K AAG
K AAA	C HGC	I ATT	D GAT	Q CAG	K AAG	K AAG	D GAC
L TTG	L	K AAA	D GAC	C HCC	S AGC	A GCC	Q CAG
FLLT	m L TTG	S TCT	S TCT	P	$^{ m Y}$	P CCT	S TCT
R CGG	S AGC	F TTC	K AAG	S	S TCG	S	D GAC
Q CAG	Q CAA	H H T C	L CTC	S	F T T T	D GAC	O CAA
F TTC	I ATT	P CCT	T ACC	S TCA	GGG	L CTG	L CTA
N AAT	L CTG	H CAT	P	V GTT	V GTG	G	E GAG
MATG	D GAT	C TGC	V GTT	W TGG	F	S TCG	K AAA

Fig. 1

and Miles (1884)

Title: "13245, A Novel Human Myotonic Dystrophy Type Protein Kinase and Uses Therefor"
Inventors: Rosana Kapeller-Libermann et al.
U.S. Patent Appl. No.: Not Yet Assigned
Everese Mail # FI 01603645111S Attorney Docket No. 10147-57111 Cust # 570

O.O. I within I	pp	
Express Mail # EL916936451US	S Attorney Docket No. 10147-57U1 Cust # 570	)

		·••					
495 1485	515 1545	535 1605	555 1665	4/25 5/25 1/25	595 1785	615 1845	635 1905
A	S	A	Q	L	A	D	Q
GCC	AGT	GCA	CAG		GCT	GAT	CAG
K	C	K	E	D	CHI	K	Q
AAG	TGC	AAA	GAG	GAT		AAG	CAG
L	E	D	K	E	R	A	E
CTG	GAA	GAC	AAA	GAG	CGG	GCT	GAG
E	T	D	I	E	S	K	A
GAG	ACA	GAT	ATC	GAA		AAG	GCT
V	I	E	E	L	E	L	N
GTG	ATC	GAG	GAA	TTG	GAG	TTG	AAT
E	Y	Q	Q	Q	R	L	I
GAG	TAC	CAG	CAA	CAG	AGA	CTG	ATC
K AAG	T ACC	S TCC	CIC	N AAT	L	K AAA	K AAG
Q	A	V	K	M	E	H	E
CAG	GCT	GTG	AAG	ATG	GAG	CAT	GAG
S	L	E	R	M	S	Q	$\Gamma$
AGT	CTT	GAG	CGG	ATG	TCT	CAG	
CIT	D	M	S	L	E	C	K
	GAC	ATG	AGC	TTG	GAA	TGT	AAA
V	Q	R	Q	R	Y	E	A
GTG	CAG	CGG	CAG	AGG	TAC	GAA	GCG
A	E	A	E	M	L	T	Y
GCT	GAG	GCA	GAG	ATG	CTC	ACA	TAT
E	L	Q	R	E	D	A	E
GAG		CAA	AGA	GAA	GAT	GCG	GAA
V	CIC	E	I	E	S	K	G
GTG		GAG	ATC	GAA	AGT	AAA	GGA
E	S	L	D	V	R	R	V
GAG	TCC	TTG	GAT	GTG	CGG	CGG	GTG
S	R	S	H	Q	R	K	E
TCA	AGA	AGT	CAT	CAA	AGA	AAG	GAA
V GTG	Q CAG	R CGA	L	A GCT	R AGA	F TTC	PCCT
R	T	K	L	Q	A	E	K
AGA	ACT	AAG		CAG	GCA	GAA	AAG
R	E	L	Q	Y	S	E	GGG
CGG	GAG	TTA	CAG	TAC	TCA	GAA	
H CAT	STCT	S AGC	CIG	E	V GTC	A GCT	Q CAA

Fig. 1D

വവ	2 2	N N	D D	5/25 ເກີເກີ	2 2	വവ	വ
65 196	67 202	69 208	71 214	73	75	77	79
R	V	E	M	H	D	H	A
AGG	GTG	GAG	ATG	CAC	GAC	CAC	GCT
E	L	M	Q	Q	L	R	N
GAG	CTG	ATG	CAG	CAG	TTG	AGA	AAT
A	K	TACC	Q	A	V	Q	I
GCC	AAG		CAG	GCC	GTG	CAG	ATC
R	K	E	I	S	K	M	MATG
CGA	AAG	GAG	ATC	TCA	AAA	ATG	
E	R	L	Q	V	I	M	A
GAG	AGA	CTA	CAG	GTC	ATT	ATG	GCG
K	I	R	Q	Q	K	N	K
AAG	ATC	AGA	CAA	CAA	AAG	AAC	AAG
A	GGC	K	S	A	E	E	Q
GCA		AAG	TCC	GCC	GAA	GAG	CAG
A	E	V	K	E	E	L	E
GCT	GAA	GTA	AAA	GAG	GAG	CTG	GAA
K	S	K	T	R	Y	T	S
AAG	TCT	AAG	ACA	CGG	TAT	ACA	AGC
E	S	N	Q	H	H	E	L
GAG	TCT	AAC	CAG	CAT	CAC	GAG	
$\Gamma$	D	E	I	K	Q	K	I
	GAT	GAG	ATC	AAA	CAG	AAG	ATT
K	E	L	D	E	E	D	K
AAA	GAG		GAC	GAG	GAG	GAC	AAA
E	R	S	D	E	K	A	G
GAG	CGA	TCT	GAT	GAA	AAA	GCT	GGC
Q	N	H	K	L	Q	L	K
CAA	AAC	CAT	AAG		CAG	CTG	AAG
L	O CAG	R CGC	CIG T	E	K AAA	D GAC	E GAG
E	L	R	R	L	L	K	H
GAG	CIG	CGC	AGA		CTG	AAA	CAT
Q	K	E	N	I	H	K	A
CAG	AAG	GAA	AAC	ATT	CAC	AAG	GCC
I	E	E	E	K	V	I	E
ATT	GAG	GAG	GAA	AAA	GTG	ATA	GAG
K	L	A	R	D	E	Q	E
AAA		GCT	AGA	GAT	GAA	CAG	GAG
L	E GAG	E GAA	R	A GCT	L CTA	N AAT	E GAG

Fig. 1E

815 2445	835 2505	855 2565	875 2625	6/25 5 5 8 8 9 7	915 2745	935 2805	955 2865
K	I	Q	N	K	Q	TACA	R
AAA	ATT	CAG	AAT	AAA	CAG		AGA
N	M	A	K	Q	S	K	H
AAT	ATG	GCC	AAG	CAG	TCA	AAG	CAT
A	E	E	D	E	E	A	A
GCC	GAG	GAG	GAC	GAG	GAG	GCG	GCA
E	E	T I C	S	E	R	Q	T
GAA	GAA		AGT	GAG	CGC	CAG	ACG
S	Q	K	H	H	E	R	L
TCT	CAA	AAG	CAC	CAC	GAG	CGC	
L CTG	A GCC		D GAC	E GAG	Q CAG	CIT	A GCA
E	K	A	Q	L	L	Q	Q
GAA	AAG	GCT	CAA	CTA	CTG	CAG	CAG
V	M	Q	H	S	S	S	I
GTG	ATG	CAG	CAC	AGT	TCC	AGC	ATC
I	N	T	S	V	L	E	E
ATT	AAC	ACA	AGC	GTC		GAG	GAG
R	R	E	I	E	Q	L	E
AGG	AGG	GAG	ATC	GAG	CAG	CIG	GAG
Q	Q	L	K	R	L	A	E
CAG	CAA		AAG	CGG	CIA	GCC	GAA
E GAA	TACC	Y TAC	E GAG	m L TTG	E GAG	A GCG	A GCT
L	FTTT	F T T T	L	R AGA	T ACA	R CGG	E GAA
S	L	K AAA	Q CAG	T ACA	CHC	A GCA	A GCA
R	S	Q	E	E	Q	A	T
AGA	AGT	CAG	GAG	GAG	CAG	GCT	ACA
I	S	Q	E	L	R	Q	T
ATC	AGC	CAA	GAG	CTG	CGC	CAG	ACC
K	N	R	L	E	K	L	E
AAG	AAT	AGG		GAA	AAG	CTG	GAG
S TCC	A GCA	CIC	K AAA	L CIG	CIC	A GCC	E GAA
D	A	E	R	L	E	T	L
GAT	GCA	GAA	CGA	CTG	GAG	ACA	CIG
M ATG	L	STCT	N AAC	R CGG	L CTG	L TTG	E GAG

Fig. 1F

975 2925	9995 2985	1015 3045	1035 3105	7/25 5918 8165	1075 3225	1095 3285	1115 3345
$\Gamma$	Y TAC	S AGT	K AAG	$_{ m ITG}$	V GTC	D GAC	V GTG
D GAC	H H H H G	R CGA	Q CAG	D GAT	S AGC	L	V GTG
T	N	L	S	M	R	M	Q
ACA	AAC		AGC	ATG	AGG	ATG	CAG
I	Q	Q	T	V	W	R	R
ATC	CAA	CAA	ACC	GTC	TGG	AGA	CGC
V	N	V	CTT	Q	A	Q	S
GTA	AAC	GTA		CAG	GCC	CAG	TCT
T	N	I	Q	E	E	CIG	E
ACT	AAC	ATT	CAG	GAA	GAG		GAG
CHU	CIC	E GAG	M ATG	E GAG	W TGG	EGAG	T ACC
S	E	D	E	$\Gamma$	Q	R	I
AGC	GAA	GAC	GAG		CAG	CGA	ATC
N	A	N	R	M	R	V	R
AAC	GCT	AAC	CGA	ATG	CGG	GTT	CGG
R	N	A	E	T	E	R	Q
CGT	AAC	GCC	GAA	ACC	GAG	CGG	CAG
CTT	D	G	T	C	K	C	D
	GAC	GGC	ACG	HGC	AAA	TGT	GAT
A	E	S	I	T	E	E	A
GCT	GAG	TCT	ATC	ACG	GAA	GAG	GCC
D GAT	T ACC	A GCT	E GAG	TACC	L CIA	F	R AGA
F TTT	L	E GAG	R CGG	K AAG	L	Q CAG	A GCG
K	Q	D	R	$\Gamma$	E	S	R
AAA	CAG	GAT	CGC		GAG	TCC	AGG
R CGC	N AAC	CIC	CIC	A GCT	D GAT	K AAA	S AGC
Q	L	Q	H	E	N	E	Q
CAG	CTA	CAA	CAT	GAG	AAC	GAG	CAG
I	Q	K	D	M	L	D	K
ATC	CAG	AAA	GAC	ATG	CTA	GAT	AAA
E GAA	E GAG	S	V GTG	T ACG	A GCC	GGT	E GAG
D GAT	E GAG	L	E GAA	Q CAA	E GAG	L	T ACC

Fig. 16

				8 / 25			
1135	1155	1175	1195	1215	1235	1255	1275
3405	3465	3525	3585	3645	3705	3765	3825
E	A	K	H	T	K	K	A
GAG	GCT	AAA	CAC	ACA	AAG	AAA	GCT
K	H	CIC	N	K	E	A	P
AAA	CAT		AAT	AAG	GAA	GCC	CCT
CIC	K AAG	E GAG	K AAA	L	H CAT	Q CAA	D GAC
A	K	R	Q	L	S	L	E
GCT	AAG	CGA	CAG	CTA	TCT		GAG
Q CAG	E GAG	E GAA	L	D GAT	$\mathbf{Y}_{\mathbf{TAT}}$	F TTT	K AAA
Q	L	T	D	A	L	D	R
CAG	CTG	ACT	GAC	GCT		GAT	GG
L	D	E	M	R	V	I	R
CTG	GAC	GAG	ATG	CGG	GTT	ATT	CGA
A	N	L	Q	D	Q	L	S
GCT	AAT	CTG	CAG	GAT	CAG		AGT
L	CIC	K AAG	Q CAG	L CIA	I ATT	K AAA	F TTT
I	K	Q	Q	A	N	T	L
ATT	AAG	CAG	CAG	GCT	AAC	ACC	TTA
E	D	O	L	E	E	Q	GGT
GAG	GAC	CAG	TTA	GAA	GAA	CAA	
A	S	L	K	Q	L	Q	K
GCT		TTA	AAA	CAA	CTG	CAA	AAG
K AAG	L	S AGC	A GCC	CIG	Q CAG	SHCH	K AAA
H	S	R	Q	G	$rac{Y}{TAT}$	I	K
CAC	AGC	CGA	CAA	GGA		ATT	AAG
E	E	A	E	Q	E	T	K
GAG	GAG	GCC	GAG	CAA	GAG	ACT	AAA
K AAG	A GCC	N AAT	E GAA	T ACT	L	U U U	A GCT
V	K	M	L	L	D	E	P
GTG	AAG	ATG	CIG	CIG	GAC	GAA	CCT
A GCA	L	E GAA	L	R CGT	S AGT	M ATG	Q CAA
$_{ m CTG}$	K AAG	L	R AGG	T I C	R AGA	K AAA	D GAC
E	Q	M	Q	I	E	V	M
GAG	CAG	ATG	CAG	ATT	GAA	GTG	ATG

## Fig. 1F

E .
£.,
in the second
and the second
<b>3</b>
<b>#</b>
а,

### Fig. 1

1455 4365	1475 4425	1495 4485	1515 4545	10/25 4 605 4 605 4	1555 4665	1575 4725	1595 4785
K AAA	W TGG	V GTC	P CCG	GGT	L	P CCC	L TTG
D GAC	ტ ტტტ	I ATT	R AGG	V GTT	L	L	V GTC
R	E	YTAC	Q	A	K	T	N
CGT	GAA		CAG	GCC	AAA	ACG	AAT
C TGC	L	K AAG	G GGA	G GGT	A GCT	C HCC	L
FTTC	H	R	A	H	D	N	A
	CAC	AGG	GCT	CAT	GAT	AAC	GCC
A	TIG	D	E	I	A	M	Y
GCC	TIG	GAC	GAA	ATT	GCT	ATG	TAC
E	S	W	R	S	E	D	CIC
GAG	AGC	TGG	AGA	TCT	GAA	GAC	
T	S		A	V	A	L	GGG
ACC	AGC	GGC	GCC	GTA	GCA	CTA	
F	S	Q	E	D	K	R	E
TTC	AGC	CAA	GAA	GAT	AAA	CGT	GAA
H	P	Q	N		E	D	E
CAC		CAG	AAT	GGG	GAA	GAC	GAG
T	E	G	D	D	A	D	T
ACA	GAG	GGA	GAC	GAC	GCA	GAT	ACC
A	K	R	Y	P	K	G	9
GCC	AAG	CGA	TAT		AAA	GGT	9
Y	T	K	I	L	A	E	V
TAT	ACC	AAA	ATT		GCC	GAA	GTG
E GAA	Q CAG	N AAC	CIC	C TGC	T ACA	L	L TTG
A GCT	L	N AAT	V GTC	L	N AAT	K AAA	V GTG
P CCT	GGT	R AGG	K AAA	E GAG	A GCA	L	V GTG
T I I	P CCA	P	S TCA	F	L	L	Q CAG
U U U	S	V GTG	G GGA	E GAA	E GAA	S	D GAC
C	N	K	E	E	S	N	S
H GC	AAC	AAG	GAG	GAA		AAC	AGT
T ACC	MATG	M ATG	L	V GTG	A GCT	GGA	F

### Fig. 1.

	•			11/25			
1615	1635	1655	1675	1695	1715	1735	1755
4845	4905	4965	5025	5085	5145	5205	5265
K AAG	V GTG	CCC	GGG	CIC	F TIC	Y TAC	A GCC
I	D	S	N	N	H	Q	A
ATC	GAC	TCA	AAC	AAC	CAC	CAG	GCC
I	V	I	E	E	I	K	F
ATT	GTG	ATC	GAG	GAA	ATC	AAG	
Y	CTT	D	I	N	C	M	V
TAT		GAC	ATT	AAC	TGT	ATG	GTG
I	C	PCCC	K	Y	S	D	A
ATT	TGT		AAG	TAC	AGC	GAC	GCT
Q	L	Q		R	C	I	P
CAA	CTG	CAG	GGC	CGC	TGC	ATC	
F	A GCA	A GCC	A GCA	L	P	E GAA	A GCA
V	R	P		I	E	Y	$\Gamma$
GTC	CGG	CCT	GGG	ATT	GAG	TAC	
A	E	L	F	V	S	F	S
GCA	GAG	CIG		GTC	TCA	TTC	TCC
G	E	H	$rac{ ext{L}}{ ext{TTG}}$	V	T	K	H
GGA	GAA	CAC		GTC	ACC	AAA	CAT
I	G	S	H	K	E	N	D
ATT	GGA	TCC	CAC	AAA	GAG	AAT	GAC
G	A	Q	C	S	I	TACC	N
GGA	GCA	CAG	TGC	AGC	ATA		AAT
P	I	A	G	P	E	G	K
CCA	ATA	GCC	GGC	CCC	GAG	GGA	AAG
V	M	L	K	M	K	I	D
GTC	ATG		AAG	ATG	AAA	ATT	GAT
H CAT	L	S TCC	V GTC	A GCC	R CGG	CIC	L
T	L	Q	A	A	I	I	F
ACC	CTA	CAG	GCT	GCA	ATC	ATC	
$_{ m CTA}$	K	K	E	C	C	S	E
	AAG	AAA	GAA	TGT	TGC	AGT	GAA
S TCC	E GAG	V GTG	F TTT	I ATC	$^{ m Y}$	$^{ m Y}$	E GAG
N	L	K	I	C	K	N	L
AAC	CTG	AAA	ATT	AGC	AAA	AAT	
K	D	K	N	L	S	T	T
AAA	GAC	AAG	AAC		AGC	ACC	ACG

Title: "13245, A Novel Human Myotonic Dystrophy Type Protein Kinase and Uses Therefor"
Inventors: Rosana Kapeller-Libermann et al.
U.S. Patent Appl. No.: Not Yet Assigned E

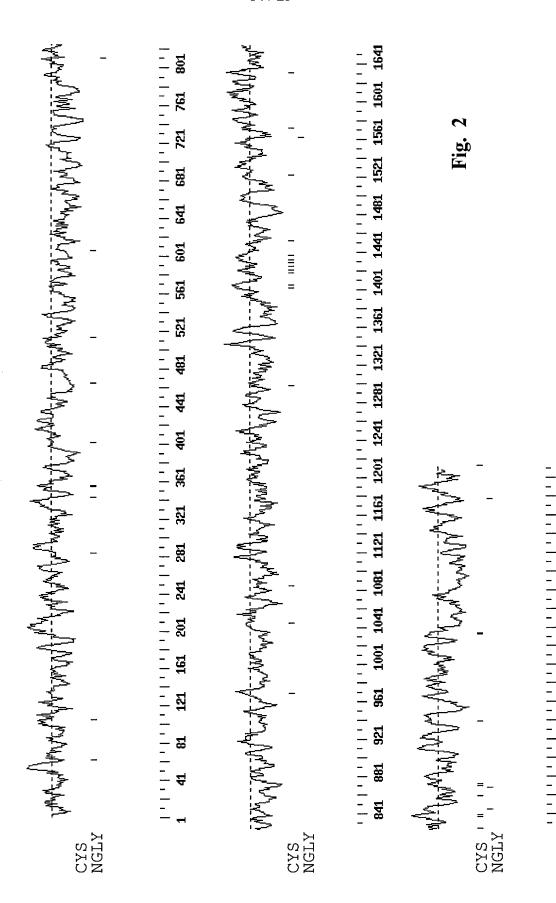
Express Mail #	EL916936451US	Attorney Docket No.	10147-57U1	Cust # 570

	•			Ť			
1775 5325	1795 5385	1815 5445	1835 5505	12/25 55 95 1	1875 5625	1895 5685	1915 5745
E	R	L	G	S	K	S	S
GAG	CGC	CIG	GGG	TCC	AAG	AGC	TCC
E	S	Y	A	I	C	R	A
GAG	AGC	TAT	GCA	ATT	TGC	CGC	GCC
R	R	P	S	A	C	S	V
CGA	CGT		TCA	GCC	TGC	TCC	GTG
Q	R	E	S	PCCT	I	T	R
CAG	AGA	GAA	TCC		ATT	ACC	CGC
GGG	G GGA	R AGA	R CGC		V GTC	S TCC	K AAG
A	Y	Y	A	L	R	P	T
GCA	TAC	TAC	GCA	CTG	AGG		ACC
S	S	A	Q	Y	$_{ m L}$	G	I
AGC	TCT	GCC	CAG	TAC		GGC	ATC
N	D	F	I	R	K	R	H
AAC	GAT		ATC	CGC	AAA	CGG	CAC
V	V	A	E	PCCG	D	H	E
GTG	GTG	GCC	GAG		GAT	CAC	GAG
Q CAG	F	$_{ m L}$	I ATT	N AAC	Q CAG	H CAC	N AAC
V	V	P	V	P	Y	E	Y
GTG	GTG		GTA	CCG	TAC	GAA	TAC
I	G	L	E	I	S	T	T
ATC	GGA	TTA	GAA	ATC	TCA	ACT	ACG
S TCA	F TTT	R CGC	L	D GAC	S TCC	G GGC	P
V	E	S	S	L	A	S	P
GTC	GAA	AGT	TCA	CTG	GCG	TCC	CCA
P CCT	H CAC	W TGG	N AAC	$^{ m Y}$	$_{ m TTG}$	E GAG	g GGC
${ m F}$	F TTC	K AAG	F	A GCG	Y TAC	K AAG	R CGA
S	C	CIC	H	R	I	V	K
AGC	TGT		CAC	CGA	ATT	GTG	AAG
N	L	D	T	A	A	CIC	N
AAC	CTG	GAT	ACC	GCC	GCG		AAC
S TCC	L	D GAC	V GTG	P	GGA	N AAC	P CCC
ST	Y	T	F	T	S	G	S
	TAC	ACA	TTT	ACC	TCA	GGA	AGC

Title: "13245, A Novel Human Myotonic Dystrophy Type Protein Kinase and Uses Therefor"
Inventors: Rosana Kapeller-Libermann et al.
U.S. Patent Appl, No.: Not Yet Assigned
Express Mail # EL916936451US Attorney Docket No. 10147-57U1 Cust # 570

S AGC	P CCA	A GCG	P CCG	P CCC	E GAA	GGC	PCCC	S AGC	H CAC	P CCG	R CGA	E GAG	P CCA	S AGC	T ACA	P	H CAC	R CGC	Y TAC	1935 5805
R CGC	EGAG	GGG	R CGG	TACC	E GAG	L	R GGC A	R AGG	D GAC	K AAG	STCT	P CĆT	9 667	R CGC	P CCC	L CTG	E GAG	R CGA	E GAG	1955 5865
K AAG	S TCC	P	G GGC	R CGG	M ATG	CIC	S AGC	T ACG	R CGG	R AGA	E GAG (	R CGG	Ω CC C	CCC	G GGG	R AGG	L CIG	F TTT	E GAA	1975 5925
D GAC	S AGC	S AGC	R AGG	GGC	R CGG	CIG	PCCT	A GCG	G GGA	A GCC	VGTG	R AGG	T ACC	P CCG	L CIG	S TCC	Q CAG	V GTG	N AAC	1995 5985
K AAG	G GGA	R AGA	G GGG	Q CAG	S AGT	A S GCC TCT	S	Q CAA	V GTT	F	T ACG	V GTT	N AAC	TACT	VGIC	T ACC	Y TAT	Y TAT	D GAC	2015 2015 6045 6045
W TGG	N AAT	K AAA	K AAG	L CTG	D GAC	N AAC	L	P CCA	A GCT	N AAC	WTGG	S TCA	V GTC	L CTG	R AGG	I ATC	I ATC	Q CAG	L	2035 6105
N AAT	N G E I R Q Q V AAT GGA GAA ATC CGG CAG CAG GTT	E GAA	I ATC	CG G	Q CAG	O CAG	V GTT	E GAA	K AAG	s TCT	V GTT	L CTG	R AGA	T ACA	D GAT	$rac{Y}{TAT}$	C TGC	* TGA		2053 6162
GCAC GAAZ CCAT	GCAGAGTTCATGTGACTTCTAGACGTGGTGACTTAAAAATGGCCTTAAGGCTGCAGACCAGCCACCTCTGTTACAA AAAGAGTTCATGGAGCACTGTAAGAAACAATTGTAAAACCTCATCTAGAAATCAGAAAGCTTCTAATTTCTATA GAAATGACCTCCCTGGAGCCGAGAGACAATCTGTTGTTGATTTTGAAGGACAGGCAAGACCAACACTGTATTTAGTT CCATAGCCAGGCCTCAACAGGGACAAGTGGCTGGCCTTAAAAACACACAGATGAGGAAATGAGGAAATGTGGCCTCAGTC CCATAGCCAGGAATTTTACTGGCAAAGGAGTTAGCATTTTTTTT	CATCACTANTANTANTANTANTANTANTANTANTANTANTANTANT	GTGA( AGTG( TCCC! CCTC!	CTTC. CACA. IGGA( AACA(	TAGACI TGACI SCCGZ SGGAC	CGTGC CGTAZ AGAGZ CAAGT	STGACACACACACACACACACACACACACACACACACACAC	TTTAF CCAAT CCTGT CGGCC	AAAAA TTGTT TTGTT	AAAAC AAAAC AAAAC	CCTTP CCTCP CTTGP CACAC	AAGGC ATCTP AAGGP SAGAT	TGCAAACAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	AGAGG TCAG CCAAG	CAGC	CACC CTTC ACAC	TCTG TAAT TGTA TGGC	SCTTACAA TTTCTATA TTTAGTT CCTCAGTC	CAA ATA GTT GTC	

# Fig. 1M



13245 AAC72823	1 MLKFKYGARN MLKFKYGVRN	PLDAGAAEPI PPEASASEPI	ASRASRLNLF ASRASRLNLF	FQGKPPFMTQ FQGKPPLMTQ	50 QQMSPLSREG QQMSALSREG
AAC27933	•	•	•	•	•
P49025	•		•	•	•
014578	•	:	•	:	•
	51				100
13245	ILDALFVLFE	ECSQPALMKI	KHVSNFVRKY	SDTIAELQEL	QPSAKDFEVR
AAC72823	MLDALFALFE	ECSQPALMKM	KHVSSFVQKY	SDTIAELREL	QPSARDFEVR
AAC27933	•			•	
P49025	•	•	•	•	
014578	•		•	•	•
	101				ر بر
13245	SLVGCGHFAE	VOVVREKATG	DIYAMKVMKK	KALLAOEOVS	FFEEERNILS
AAC72823	SLVGCGHFAE	VQVVREKATG	DVYAMKIMKK		FFEEERNILS
AAC27933	•	•	•	•	•
P49025	•	•	•	•	•
014578	•	•	•	•	•
$\leftarrow$	151				200
13245	RSTSPWIPQL	QYAFQDKNHL	YLMEEYQPGG	DLLSLLNRYE	DQLDENLIQF
AAC72823	RSTSPWIPQL	QYAFQDKNNL	YLVMEYQPGG	DFLSLLNRYE	DQLDESMIQF
AAC27933	•	•	•	•	•
P49025	•	•	•	•	•
014578	•	•	•	•	•

450 PAKTSSMEKK PAKVSSMEKK PAKVSSMEKK	500 VELKASETQR	VELKASETQR VELKASETQR VELKASETQR		550	DIREQSRKLQ DIREQSRKLQ	DIREQSRKLQ DIREQSRKLQ		009	ESKLAAEEFK ESKLAAEEFK	ESRLAAEEFK	ESRLAAEEFK	•
SESVVSGLDS SESVVSSLDS SESVVSSLDS	EVEAVLSQKE	EVEAVLSOKE EVEAVLSOKE EVEAVLSOKE			EDDKALQLLH EDDKALQLLH	EDDKALQLLH EDDKALQLLH	•		KSULIESELK RSDLYESELR	RSDLYESELR	RSDLYESELR	•
YSKALGILGR YSKALGYLGR YSKALGYLGR	EMTRLHRRVS	EMTRLHRRVS EMTRLHRRVS EMTRLHRRVS			LEQARMEVSQ LEQARMEVSQ	LEQARMEVSQ LEQARMEVSQ	•		LEEDLVSARR	LEEDLVSARR	LEEDLVSARR	•
GEELPFVGFS GEELPFVGFS GEELPFVGFS	SODKCHKMEQ	SQDKCHKMEQ SQDKCHKMEQ LLGEEAMMEQ			ITECSSLKRS ITECSSLKRS	ITECSSLKRS ITECSSLKRS	•		VEEMKLMMNQ VEEMRLMMNQ	VEEMRLMMNQ	VEEMRLMMNQ	•
DOUSPSGES CVPAEPLAFS VCQLSPSGES	51 LLIKSKELOD	LLIKSKELQD LLIKSKELQD	•	01	SLLEQDLATY SLLEQDLATY	SLLEQDLATY SLLEQDLATY	•	51	EIKEQEYQAQ EIKEOEYOAO	EIKEQEYQAQ	EIKEQEYQAQ	•
13 13 13 14 14 14	78 45 45			5	4.0	AAC27933 P49025	1457		13245 AAC72823	93	302	014578

650	LQEKLEKA	LQEKLEKAVK	LQEKLEKAVK	LQEKLEKAVK	•	700	VEAEERRHSL	VEAEERRHSL	VEAEE	VEAEERRHSL	:	750	KHRFAOVSAO	KHREAOVSAO	KHREAOVSAO		KHKEAQV SAQ	•	800	HEEEAHEKGK	HEEEAHEKGK	HEEEAHEKGK	HEEEAHEKGK	HEEEAHEKGK
	NAEQQLKIQE	NAEQQLKIQE	NAEQQLKIQE	NAEQQLKIQE	•		DSSEGIRKKL	DSSEGIKKKL	DSSEGIKKKL	DSSEGIKKKL	•		MADKTT.F.T.F.F.	MADKILELEE		111111111111111111111111111111111111111	MADKILLEL	•		KETLENMMQR	KESLENMMOR	KESLENMMQR	KESLENMMOR	KETLENMMOR
	VGEYAKLEKI	VGEYSKLEKI	VGEYSKLEKI	VGEYSKLEKI			RELEKLONRE	RELEKLHNRE	RELEKLHNRE	RELEKLHNRE	•		TOTKSOOTOO	TOTKSEOTOO	K +	· ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) (	TOTESHIDE			DNQIKKDLAD	DNQIKKDLAD	DNQIKKDLAD	DNQIKKDLAD	DNQIKKDLAD
	LKAKDQGKPE	MKAKDQGKPE	MKAKDQGKPE	MKAKDQGKPE	•		AKERAE	NIRQAKERAE	NIRQAKERAE	NIRQAKERAE	•		TRRENET KDD	ERRENRI,KDD			EKKENKLKUU	•		QHYEEKIKVL	QHYEEKIKVL	QHYEEKIKVL	QHYEEKIKVL	7V
0.1	RKATECQHKL	RKANECQHKL	RKANECQHKL	RKANECQHKL	•	51	•	ASTEATELLO	ASTEATELLO	ASTEATELLO	•	01	TNKVKRT.FTM	FNKVKRIFTM			ENKVKKLETM	•	51	HLEVHLKQKE	HLEVHLKQKE	HLEVHLKQKE	HLEVHLKQKE	•
09	324	282	793		157	9	324		93		1457	7	, , ,	0 1 2 C 1 2	7 0	) (	02	1457	7	3245	282	93	9	1457

850	QRNMKAQEEM QRNMKAQEEM	QRNMKAQEEM	QRNMKAQEEM	QRNMKAQEEM	006	NRLLELETRL	SRLLELETRL	SRLLELETRL	SRLLELETRL	NRLLELETRL	950	ALESQLRQAK	ALESQLRQAK	ALESQLRQAK	ALESQLRQAK	ALESQLRQAK	1000	LEEQLNQLTE	TEEOLNOLTE	TEEOLNOLTE	LEEQLNQLTE	LEEQLNQLTE
	KLAANSSLFT KLAANSSLFT	KLAANSSLFT	KLAANSSLFT	KLAANSSLFT		KISHQDHSDK	KISHQDHSDK	KISHQDHSDK	KISHQDHSDK	KISHQDHSDK		QLTALQAARA	QLTALQAARA	QLTALQAARA	QLTALQAARA	QLTALQAARA		LRNSCTVITD	LRNSCTVITD	LRNSCTVITD	LRNSCTVITD	LRNSCTVITD
	QRIVELSEAN QRIVELSEAN	QRIVELSEAN	QRIVELSEAN	QRIVELSEAN		QNRKLEEQLE	QNRKLEEQLE	QNRKLEEQLE	QNRKLEEQLE	QNRKLEEQLE		LQLSLQERES	LQLSLQERES	LQLSLQERES	LQLSLQERES	LQLSLQERES		RDEIQRKFDA	RDEIQRKFDA	RDEIQRKFDA	RDEIQRKFDA	RDEIQRKFDA
	AMDSKIRSLE AMDSKIRSLE	AMDSKIRSLE	AMDSKIRSLE	AMDSKIRSLE		LETQAGKLEA	LETQAGKLEA	LETQAGKLEA	LETQAGKLEA	LETQAGKLEA		KLELKRQLTE	KLELKRQLTE	KLELKROLTE	KLELKRQLTE	KLELKRQLTE		EEEIQALTAH	EEEIQALTAH	EEEIQALTAH	EEEIQALTAH	EEEIQALTAH
01	ILSEQKAMIN ILSEQKAMIN		ILSEQKAMIN	ILSEQKAMIN	51	ISELRQQKFY	ISELRQQKFY	ISELRQQKFY	ISELRQQKFY	ISELRQQKFY	01	REVSLEHEEQ	REVSLEHEEQ	REVSLEHEEQ	REVSLEHEEQ	REVSLEHEEQ	51	TELEETTAEA	TELEETTAEA	TELEETTAEA	TELEETTAEA	TELEETTAEA
8(	13245 AAC72823	793	302	157	8	324	$^{\circ}$	93	P49025	457	)6	324	282	793	90	57	<u>o</u>	3245	2823	7933	025	14578

1050	TEREMQLTSQ TEREMQLTSQ	TEREMOLTSO	TEREMQLTSQ	TEREMQLTSQ	1100	VLGDEKSQFE	VLGDEKSQFE	VLGDEKSQFE	VLGDEKSQFE	VLGDEKSQFE	, ,	0611	EILALQQALK	EILALQQALK	EILALQQALK	EILALQQALK	EILALQQALK	•	1200	KORLLEEQAK	KORLLEEQAK	KORLLEEQAK	KORLLEEQAK	KORLLEEQAK
	SEVDHLRREI SEVDHLRREI	SEVDHLRREI	SEVDHLRREI	SEVDHLRREI		KERQWEAWRS	KERQWEAWRS	KERQWEAWRS	KERQWEAWRS	KERQWEAWRS			VELAVKEHKA	VELAVKEHKA	VELAVKEHKA	VELAVKEHKA	VELAVKEHKA			QOKLETEREL	QOKLETEREL	QQKLETEREL	QOKLETEREL	QOKLETEREL
	GANDEIVQLR GANDEIVQLR	GANDEIVQLR	GANDEIVQLR	GANDEIVQLR		LEALNDELLE	LEALNDELLE	LEALNDELLE	LEALNDELLE	LEALNDELLE			DORITESROV	DORITESROV	DORITESROV	DORITESROV	DQRITESRQV			AMLEMNARSL	AMLEMNARSL	AMLEMNARSL	AMLEMNARSL	AMLEMNARSL
	YLSKQLDEAS YLSKQLDEAS	YLSKQLDEAS	YLSKQLDEAS	YLSKQLDEAS		_			CIMLEEQVLD	CIMLEEQVMD			DTEKQSRARA	DTEKQSRARA	DTEKQSRARA	DTEKQSRARA	DTEKQSRARA			DKLNDLEKKH	DKLNDLEKKH	DKLNDLEKKH	DKLNDLEKKH	DKLNDLEKKH
1		DNAELNNONF	DNAELNNQNF	DNAELNNQNF	51	KQTMEALKTT	KQTMEALKTT	KQTMEALKTT	KQTMEALKTT	KQTMEALKTT		01	CRVRELQRML	CRVRELQRML	CRVRELQRML	CRVRELQRML	CRVRELQRML		51	EQKLKAESLS	EQKLKAESLS	EQKLKAESLS	EQKLKAESLS	EOKLKAESLS
100	)	C27933	49025	4578	0	3245		7933	49025	4578		$\vdash$	324	7282		4902			$\vdash$	32	282	2793	4902	1457

<u>_</u>
C)
į.
1
H
ğerin
T
₽
į.
ħ
IJ

1450	1500	1550	1600 PDKQRWVTAL PDKQRWVTAL PDKQRWVTAL
CHPKCSTCLP	WMKVPRNNKR	DGDVSIHGAV	
ASKCLECQVM	EPSSSLHLEG	PVEEFELCLP	RTLYLLAPSF
ASKCLECQVM	EPGSSLHLEG	PVEEFELCLP	RTLYLLAPSF
ASKCLECQVM	EPGSSLHLEG	PVEEFELCLP	RTLYLLAPSF
ASKCLECQVM	EPGSSLHLEG	PVEEFELCLP	RTLYLLAPSF
CLDTVHFGRQ CLDTVHFGRQ CLDTVHFGRQ CLDTVHFGRQ	KMNSPGLQTK KMNSPGLQSK KMNSPGLQSK KMNSPGLQSK KMNSPGLQSK	DNEAREAGOR DNEAREAGOR DNEAREAGOR DNEAREAGOR	SHPHTTCWPG SHPHTTCWPG SHPHTTCWPG SHPHTTCWPG
LNMRATKCAV	THFTEAFCRD	VLEGSKVLIY	A
LNMRATKCAV	THFTEAFCRD	VLEGSKVLIY	ADVPYILKME
LNMRATKCAV	THFTEAFCRD	VLEGSKVLIY	ADVPYILKME
LNMRATKCAV	THFTEAFCRD	VLEGSKVLIY	ADVPYILKME
O1	51 ATCGLPAEYA ATCGLPAEYA ATCGLPAEYA ATCGLPAEYA ATCGLPAEYA	·01	51
HNIPHRFNVG		·GQQGWDRKYI	GASELANTAK
HNIPHRFNVG		GQQGWDRKYI	GASELANTAK
HNIPHRFNVG		GQQGWDRKYI	GASELANTAK
HNIPHRFNVG		GQQGWDRKYI	GASELANTAK
140	14	15	15
13245	13245	13245	13245
AAC72823	AAC72823	AAC72823	AAC72823
AAC27933	AAC27933	AAC27933	AAC27933
P49025	P49025	P49025	P49025
014578	014578	014578	014578

1650	PFSDQVVLVG	PESDQVVLVG	PFSDQVVLVG	PFSDQVVLVG	PFSDQVVLVG	1700	GEERALCLVD	GEERALCIVD	GEENALCIVD		GEERALCLVD	1750	GLCICAAMPS	SLCICAAMPS	SICICAAMPS	SICICAAMPS	GLCICAAMPS	) ) T	1800	NKFYEIDMKQ	NKFYEIDMKQ	NKFYEIDMKQ	NKFYEIDMKQ	NKFYEIDMKQ
	DDRLDMNCTL	DDRLDMNCTL	DDRLDMNCTL	DDRLDMNCTL	DDRLDMNCTL		KDLEKLLMIA	KDLEKLLMIA	KULEKLLMIA		KDLEKLLMIA		HLFGAGKIEN	HLFAAGKIEN	HLFAAGKIEN	HLFAAGKIEN	HLFGAGKIEN			FINYSILIGT	FINYSILIGT	FINYSILIGT	FINYSILIGT	FTNYSILIGT
	LGNSLLKLEG	LGNSLLKLEG	LGNSLLKLEG	LGNSLLKLEG	LGNSLLKLEG		IGAVFQIYII	IGAVEQIYII	1GAVEQLILL	IGAVFUILL	IGAVFQIYII		PNIFEAVKGC	PNIFEAVKGC	PNIFEAVKGC	PNIFEAVKGC	PNIFEAVKGC			ETSEPCSCIH	ETSEPCSCIH	ETSEPCSCIH	ETSEPCSCIH	ETSEPCSCIH
	.EKAEADAKL	REKAEADAKL	REKAEADAKL	REKAEADAKL	REKAEADAKL		LKNSLTHVPG	LKNSLTHIPG	LKNSLTHIPG	LKNSLTHLFG	LKNSLTHVPG		SHLPAOPDIS	SHLPAOPDVS	SHLPAQPDVS	SHLPAQPDVS	SHLPAQPDIS			LSKYCIRKEI	LSKYCIRKEI	LSKYCIRKEI	LSKYCIRKEI	LSKYCIRKEI
0.1	•	ESVVAGGRVS	ESVVAGGRVS	ESVVAGGRVS	ESVVAGGRVS	51		TEEGLYALNV	TEEGLYALNV	TEEGLYALNV	TEEGLYALNV	01	VKKVKOSTAO	VKKVKOSLAO	VKKVKOSLAO	VKKVKOSLAO	VKKVKQSLAQ		51	KVVILRYNEN	KVVILRYNDN	KVVILRYNDN	KVVILRYNDN	KVVILRYNEN
160	324	7282	793	49	457	9	3245	AAC72823	2793	902	1457	7	3245	7282	793	4902	014578		17	24	7282	2793	P49025	1457

OCOT	EYLLCFHEFG	EYLLCFHEFG	EYLLCFHEFG	EYLLCFHEFG	EYLLCFHEFG	1900	VIEIQARSSA	VIEIQARSSL	VIEIQARSSL	VIEIQARSSL	VIEIQARSSA	1950	KGNLVKESGT	KGNLVKESGT	KGNLVKESGT	KGNLVKESGT	KGNLVKESGT	2000	HPREPSTPHR	HPREPSTPHR	HPREPSTPHR	HPREPSTPHR	HPREPSTPHR
	VQVNSAGQRE	VQANSAGQRE	VQANSAGQRE	VQANSAGQRE	VQVNSAGQRE		LFVTHFNSLE	LFVTHFNSLE	LFVTHFNSLE	LFVTHFNSLE	LFVTHFNSLE		YQDKLRVICC	YQDKLRVICC	YQDKLRVICC	YQDKLRVICC	YQDKLRVICC		SSPAPPEGPS	SSPAPPEGPS	SSPAPPEGPS	SSPAPPEGPS	SSPAPPEGPS
	ASSNSFPVSI	SSSNSFPVSI	SSSNSFPVSI	SSSNSFPVSI	ASSNSFPVSI		PLAFAYREPY	PLAFAYREPY	PLAFAYREPY	PLAFAYREPY	PLAFAYREPY		SSGAIYLASS	SSGAIYLASS	SSGAIYLASS	SSGAIYLASS	SSGAIYLASS		YNEHTTKRVA	YNEHITKRVA	YNEHITKRVA	YNEHITKRVA	YNEHITKRVA
	DHSLAPAVFA	DHSLAPAVFA	DHSLAPAVFA	DHSLAPAVFA	DHSLAPAVFA		RIDDLKWSRL	RTDDLKWSRL	RTDDLKWSRL	RTDDLKWSRL	RTDDLKWSRL		PNPRYLGPAI	PNPRYLGPAI	PNPRYLGPAI	PNPRYLGPAI	PNPRYLGPAI		CODNIKRCPDT	SSPNKRGPPT	SSPNKRGPPT	SSPNKRGPPT	SSPNKRGPPT
01	YTLEEFLDKN	YTLDEFLDKN	YTLDEFLDKN	YTLDEFLDKN	YTLEEFLDKN	51	VFVDSYGRRS	VFVDSYGRRS	VFVDSYGRRS	VFVDSYGRRS	VFVDSYGRRS	01		GSPARAYLEI	GSPARAYLEI	GSPARAYLEI	GTPARAYLDI	г. 1-	THEPCDOTOR	FOHRVPSTSR	EOHRVPSTSR	EQHRVPSTSR	EHHRGPSTSR
$\infty$	$\triangle 1$	32	93	)2	7	$\infty$	3245	82	2793	P4902	57	σ	3245	282	793	902	014578	0,1		0 1 2 2 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	93	902	57